Sharing targeted proteomics assays using Skyline and Panorama

Josh Eckels¹, V Sharma², B MacLean², GK Taylor¹, NJ Shulman², AB Stergachis², SA Joyner³, JD Jaffe⁴, Michael J. MacCoss²

¹LabKey Software, San Diego, CA; ²University of Washington, Seattle WA;

³Carnegie Mellon University, Pittsburgh, PA; ⁴The Broad Institute, Cambridge, MA



http://panoramaweb.org/

Overview

Panorama developers have implemented repository software for laboratories accumulating targeted proteomics experimental results in the form of Skyline documents. The software helps labs organize results, collaborate securely, and build collections of data representative of targeted assays to inform future experiments. Skyline, a popular Targeted MS desktop application, now supports both publishing a document directly to a server running Panorama, as well as downloading chromatogram libraries representative of targeted assays from a Panorama server. Developed as a module in the LabKey Server biomedical data management platform, Panorama is freely-available and open source. Free hosted Panorama projects are also available on http://panoramaweb.org.

Introduction

Data Flow Centered around Skyline

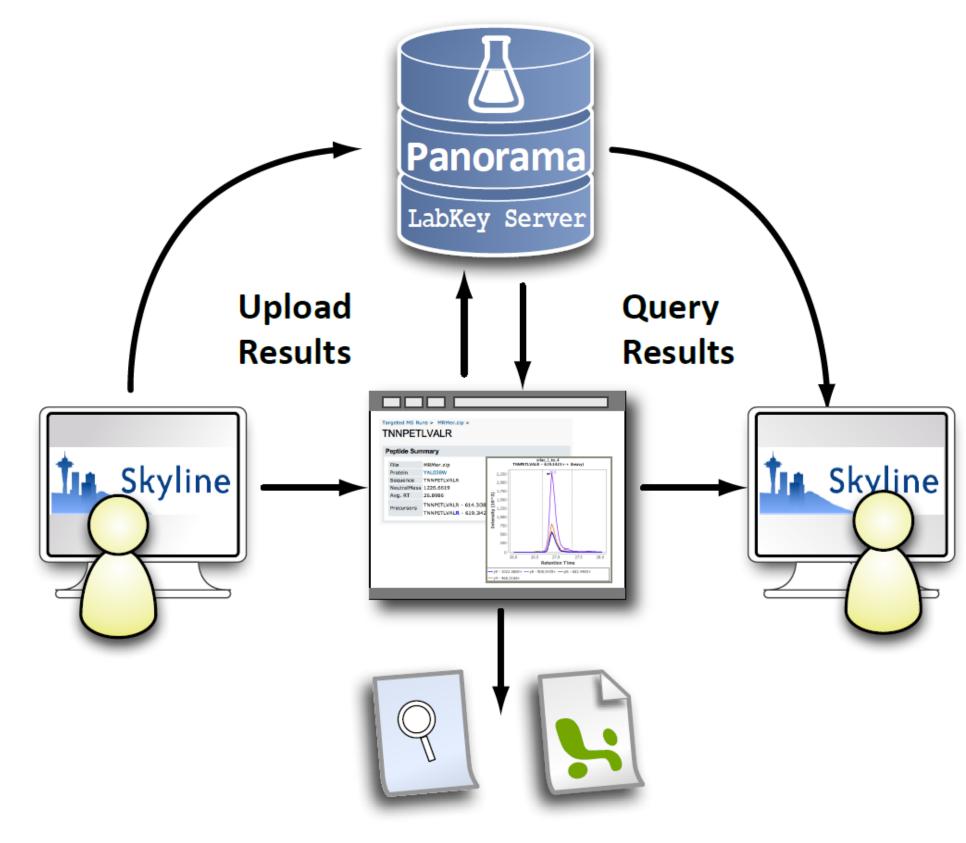


Figure 1: A typical workflow begins and ends with Skyline. Users upload data from Skyline into Panorama. It can be viewed and searched directly within Panorama, and exported back to Skyline as a shared document or a chromatogram library.

Methods

The Skyline team designed Panorama to integrate with existing Skyline targeted workflows. Investigators can publish Skyline documents to a Panorama server from within Skyline. Representative data in the repository can be stored within a library of relative peptide response for a protein, or of relative product ion response for a peptide, or both. Targeted assays stored in a Panorama server can be exported as chromatogram libraries and used in Skyline for designing new methods, or for comparing with newly acquired data. Representative data for different experimental conditions may be stored separately in different folders on the same Panorama server.

- Open source under Apache 2.0 License
- Data are stored in either Microsoft SQL server or Postgres
- LabKey Server is written in Java and JavaScript served by Tomcat

Results

1. Create Folder 2. Users / Permissions 3. Configure Targeted MS Folder Targeted MS Folder Chromatogram library - curated precursor and product ion expression data for use in designing and validating future experiments Rank peptides within proteins by peak area

Figure 2: When creating a new Panorama folder, the user selects a Targeted MS folder type of either experimental data or chromatogram library.

Publish from Skyline

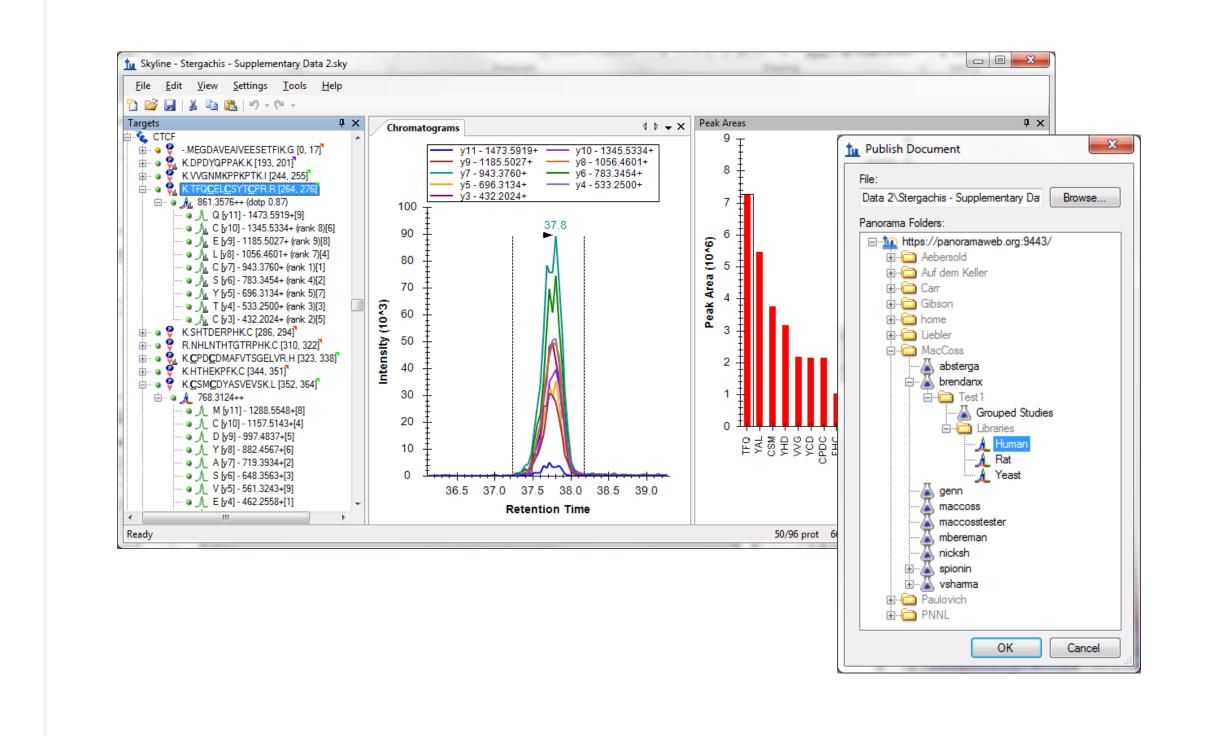


Figure 3: Results from Skyline can be published directly to Panorama or uploaded through the web interface (not pictured).

Experimental Folder View

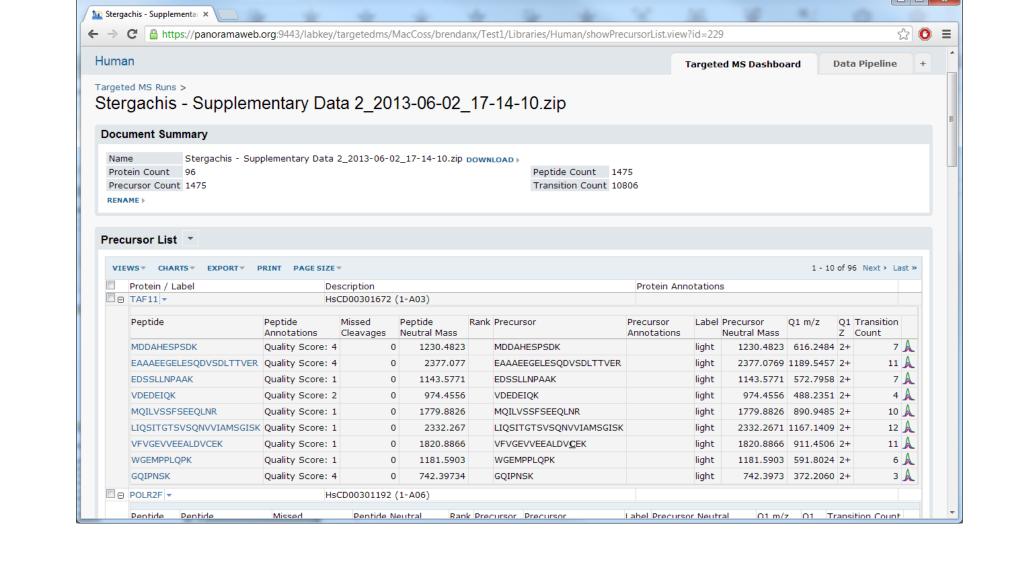


Figure 4: Uploaded data is viewable through the Panorama web interface. A DOWNLOAD link provides an easy way to inspect the data in Skyline.

Protein Detail View



Figure 5: The Protein or Peptide Group view displays sequence coverage and other information for all of the matching peptides.

Peptide Detail View

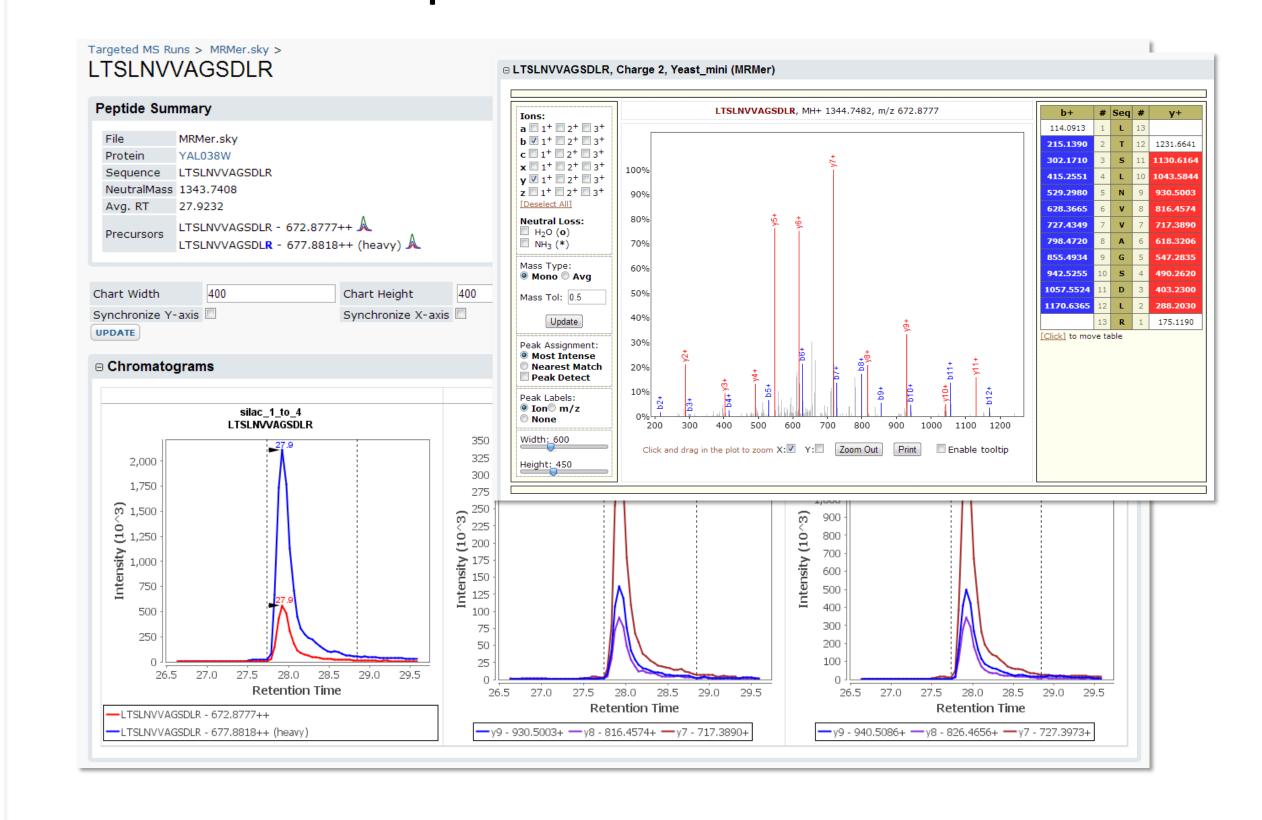


Figure 6: Detailed data about each peptide such as a library spectrum, sequence, mass, and chromatograms are displayed.

Enhanced Search Interface

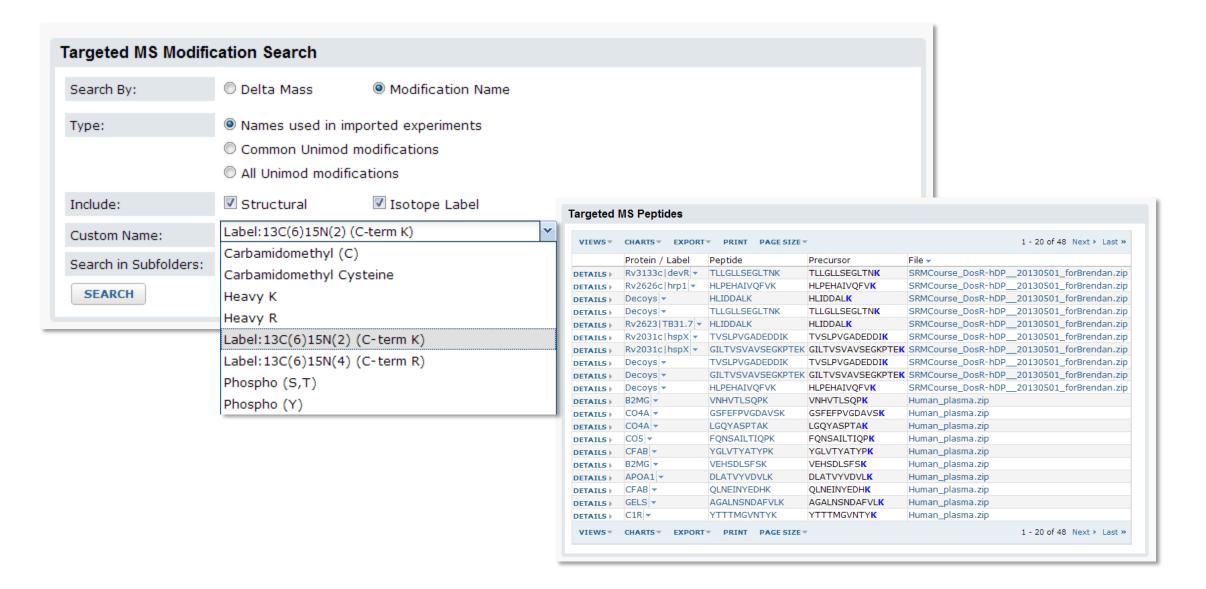


Figure 7: An enhanced search interface allows for search by protein, by peptide, or by modification name or delta mass. Above is an example search for a C-terminal modification.

Build Chromatogram Library

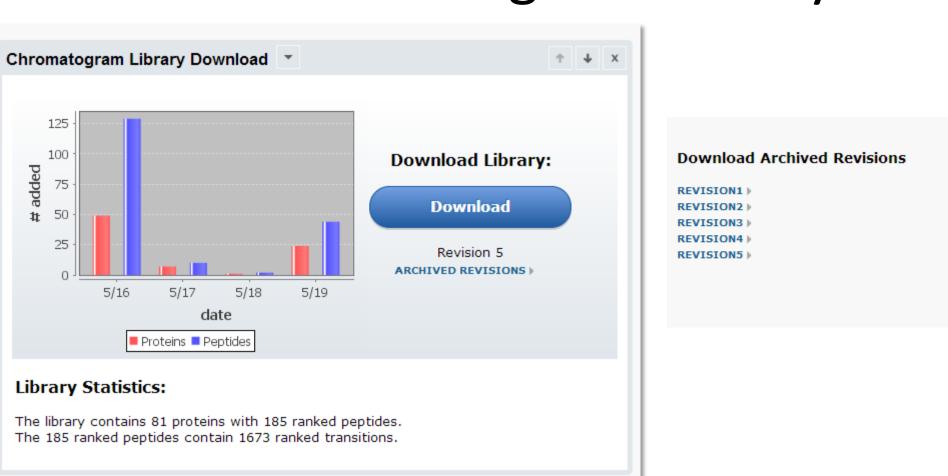


Figure 8: The chromatogram library portal provides easy access to the current library and archived revisions. It also displays statistical information about the peptides and proteins for which library chromatograms are stored.

Download Library to Skyline

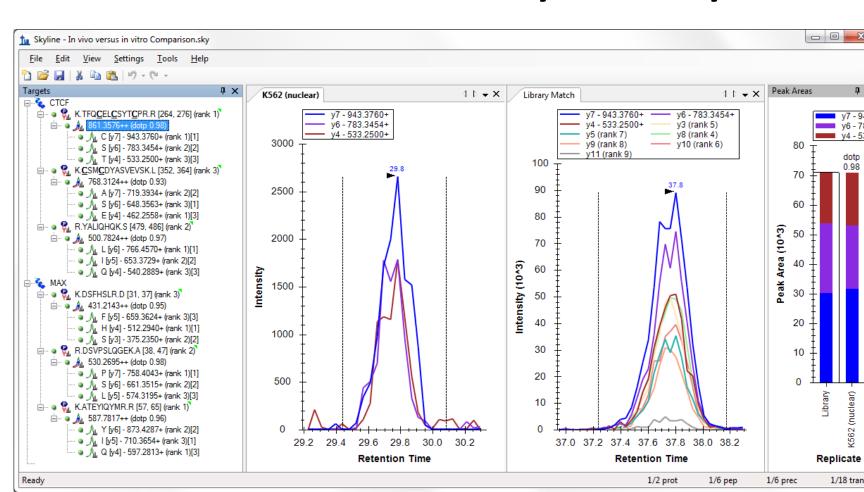


Figure 9: Chromatogram libraries containing data from many different runs may be downloaded and imported back into Skyline for use in picking best responding peptides and transitions, and validating newly collected data.

Conclusions

The development team deployed Panorama as part of LabKey Server version 12.3 in December 2012, which made it available for laboratories and organizations to install on their own servers. In addition, http://panoramaweb.org, a Panorama server hosted at the University of Washington allows investigators to request their own projects. As of June 2013, this server hosts projects for more than 20 major proteomics labs. The LabKey Server security model, at the heart of Panorama, allows fine grained control over data sharing with other individuals or the general public regardless of where the server is hosted. Panorama is being used by researchers to share data with collaborators, and to fulfill journal submission and publication requirements. Researchers and organizations are considering the use of Panorama to develop public resources for publishing targeted assays related to their research areas.

Future Work:

- Release Chromatogram Library support (July 2013)
- Support storing normalized retention times (iRT)
- Support for storing and viewing QC runs

References

(1)Stergachis AB, MacLean B, et al. Nat. Methods. 2011/08;8:1041-1043.
(2)Abbatiello SE, Mani DR, et al. Mol. Cell. Proteomics. 2013/05;10.1074/mcp.M112.027078.
(3)Glukhova VA, Tomazela DM, et al. J. Proteome Res. 2013/05;10.1021/pr400067k.
(4)Rardin MJ, Newman JC, et al. PNAS. 2013/04;10.1073/pnas.1302961110.